Reconstructing population histories and biogeography of Antarctic *Charcotia* (Amphipoda, Crustacea)

Plevoets Tim^{1,2}, Robert Henri², Kochzius Marc¹ and Schön Isa²

- Onderzoeksgroep Mariene Biologie (VUB), Pleinlaan 2, 1050 Brussel, Belgium E-mail: <u>Tim.Ingrid.Plevoets@vub.be</u>
- ² Koninklijk Belgisch Instituut voor Natuurwetenschappen, Afdeling Zoetwaterbiologie, IRScNB/KBIN, Vautierstraat 29, 1000 Brussel, Belgium

Historically, Antarctica underwent many environmental changes throughout time. Glaciation and deglaciation periods forced organisms to adapt to new conditions, undergo extinctions, or migrate. During glaciations, migrations occurred to different refugia such as the deep sea, icefree regions of the Antarctic continent and sub-polar regions. These refugia created barriers with reduced gene flow and increased diversification and speciation. Now, Antarctica is undergoing new alterations induced by global warming and ocean acidification. The RECTO (Refugia and Ecosystem Tolerance in the Southern Ocean) project investigates the historical dynamics forced by previous glaciation periods and possible responses to future climate change. One part of the project reconstructs the population history of different taxa from various trophic levels. Here, we will specifically focus on the amphipod genus Charcotia (formerly known as Waldeckia sp.), of which two species are investigated: C. obesa and C. amundseni. Both species are scavenging amphipods, and are morphologically and genetically distinct. They most likely also have different bathymetrical distributions, with C. amundseni being more abundant at larger depth. The population history and biogeography will be reconstructed from different localities in the Southern Ocean with molecular tools, including sequencing the COI DNA barcoding region, to construct haplotype networks and test for cryptic diversity. We will also apply Next-Generation-Sequencing (NGS) techniques to unravel the complete mitochondrial genome of these amphipod species. Sequence data from complete mitochondrial genomes will allow us to design primers for long-range PCRs to obtain mitogenomic data from different populations of both species. This way, phylogenies for reconstructing the evolutionary history will be statistically better supported. Possible differences in mitochondrial genomes between species could also be non-neutral and indicate specific temperature adaptations. The latter will be assessed by comparisons with mitogenomes of closely and more distantly related Crustaceans from Antarctica.

Keywords: Amphipoda; Antarctica; Population history